

**FIGURE 1****HMMGENE FOR NT\_006302.5**

Peptide VMLMIQETNK (SEQ ID NO:18, frame = 1)

Predictions :

1223361-1223403 +

1224023-1224114 + VMLMIQETNK

Score = 0.158

>NT\_006302.5

MALSLSSSKRLQLDNRVMLMIQETNKQKVKGSGPYRNMTVTQMS\*

**FIGURE 2****HMMGENE FOR NT\_006431.5**

Peptide LLNNFPYR (SEQ ID NO:20, frame = 1)

Predictions :

2323834-2323931 +

2350894-2350927 +

2351807-2351866 +

2363588-2363659 + LLNNFPYR

Score = 0.019

>NT\_006431.5

MISRQIGCRVYEDLRISKFFVISNCKDETAINGFYFGKNSIYGKVIEKTDEEIRSLFYE  
FPQTQLLNNFPYREVLSLPVPRSSDRK\*

**FIGURE 3****HMMGENE FOR NT\_007712.5**

Peptide SGCTNLRSHQQCIR (SEQ ID NO:27, frame = 3)

Predictions :

116490-116500 +

121555-121669 + SGCTNLRSHQQCIR

Score = 0.081

>NT\_007712.5

MLASNSIFHFLRTLQTVLRSGCTNLRSHQQCIRVPFSPHPQ\*

**FIGURE 4****HMMGENE FOR NT\_007914.5**

Peptide ESIYFIIAAMLVATK (SEQ ID NO:31, frame = 1)

Predictions :

1365933-1366033 +

1374991-1375117 + ESIYFIIAAMLVATK

Score = 0.137

>NT\_007914.5

MHRKDN GEMSAGEAGKAGTPKGEGHGKKPTHVISYSSSKRKSLFFWKESIYFIIAAMLV  
ATKAANQIYEGOPTQS\*

**FIGURE 5****HMMGENE FOR NT\_009891.1**

Peptide QADGTVFSK (SEQ ID NO:47, frame = 3)

Predictions :

995796-995822 +

1001710-1001787 + QADGTVFSK

Score = 0.080

>NT\_009891.1

MIKTESKSKYLSFFTSFKQADGTVFSKMKRKHLK\*

**FIGURE 6****HMMGENE FOR NT\_010909.5**

Peptide CVIFPLNSYGMLLK (SEQ ID NO:53, frame = 3)

Predictions :

146623-146704 +

164675-164798 +

176327-176399 +

177711-177772 +

183840-183972 +

184830-184912 + CVIFPLNSYGMLLK

185665-185759 +

195917-196005 +

197742-198041 +

Score = 0.000

>NT\_010909.5

MAFPDHKDAGKCSHLFSVPGEEREVKIGVPAVFCSCPCYVAELCCPILSRAPKPPDPVA  
AEHLNHGQSRSDLSAYVSTYLVPGNVLTGDPMTEDPTMERPYTFKDFLLRPRRDVSS  
ESDNNIRQINQEAHRRFRSRRHISEDLEPEPSEGGDVPEIYYHENINLGEQKCVIFPL  
NSYGMLLKTI SDQPSGAVRGTKQKASDHSRLQWGTVQLFDCWEERKDAKGRYYVNHNN  
RTTTWTRPIMQGAKDSPVRRRAVKDTLSNPQSPQSPYNPKPKQHKVTQSFLPPGWEMRI  
APNGRPFFIDHNTKTTTWVRLLLLFGSIFIMKSGINSLISLVFVVLAEELD\*



**FIGURE 9****HMMGENE FOR NT\_022148.5**

Peptide CLCTHNGASKYMK (SEQ ID NO:73, frame = 1)

Predictions :

513123-513179 +

517522-517632 +

524582-524606 +

530347-530459 + CLCTHNGASKYMK

Score = 0.033

>NT\_022148.5

MDLTLLLETHLESYRISSQMPSFLLPLGQGGSTVIRDNVDPQKRAADLQESGQTIFORKT  
KTSEEGVNSPRRHNNPKCLCTHNGASKYMKQKHTEPDTSQLY\*

**FIGURE 10****HMMGENE FOR NT\_022851.5**

Peptide EQNKILSNLEIER (SEQ ID NO:76, frame = 3)

Predictions :

187415-187484 + EQNKILSNLEIER

191445-191529 +

202588-202654 +

203509-203661 +

204036-204245 +

Score = 0.023

>NT\_022851.5

MEQDTKELKEEQNKILSNLEIERDKKEEAETQRYEIFPRTCKCYELEPECKSRYQHLSEE  
AEDMGLVVICPYLSEAAQSPQVFECIWSFLQISLVFISQNNLELVEISGKTLQDDYVTI  
ARVICDQGGRRVNFGISWKLEVRGLDRDGKSCPQDPEKDSKEQPNLTEGEKAKGAVCKN  
QISWSLASAKLLCVGRV\*

**FIGURE 11****HMMGENE FOR NT\_007897.5**

Peptide TEGLTLLQLV (SEQ ID NO:30, frame = 2)

Predictions :

1266436-1266537 + TEGLTLLQLV

Score = 0.108

>NT\_007897.5

MDKRREAGNRESRISPGRVAGGRTEGLTLLQLV\*

**FIGURE 12****HMMGENE FOR NT\_009561.5**

Peptide MKPLVDYK (SEQ ID NO:43, frame = 1)

Predictions :

800421-800456 +

802726-802910 +

803769-803924 +

813981-814042 +

820146-820240 +

833001-833030 + MKPLVDYK

Score = 0.025

>NT\_009561.5

MDMHRDKVYNEQGLIHMLFVAENEVSLEFSSLVLCFLPMKRKKEKTPDGEPQIVGRFETP  
LEFVLVMQSLVQTDNKTAFSDNFSYKSRLSDKLPSVPLPAWMHSWNLAFHKGIRIAFRQ  
CFNHPKSRMYQSSLANITVLCASFDYLFRDEEPGLSNICTFSSRLVQKVQLTATEGLLS  
IRMKPLVDYK\*

**FIGURE 13****HMMGENE FOR NT\_011387.5**

Peptide DSYLVNKR (SEQ ID NO:55, frame = 2)

Predictions :

16190762-16190828 +

16193267-16193291 +

16197014-16197074 +

16205986-16206098 +

16210646-16210725 +

16212833-16212956 +

16214152-16214188 + DSYLVNKR

Score = 0.004

&gt;NT\_011387.5

MHNSPTVVTTQYSLTDEWIIKWVMYQNRQGNCSRGSGFTFWLGDKHSVDPSIASPS  
PEAAALCVPDDNLGIGTNQYQEWVCWERALRLTRMDSINQAPLPCILSCIGAMEATALL  
RPVSCLTFRKCVDFWLRVEREIAWERKSSYECQLNFGCFYKDSYLVNKR\*

**FIGURE 14****HMMGENE FOR NT\_027064.2**

Peptide PEMVVQACSLSY (SEQ ID NO:96, frame = 3)

Predictions :

553561-553602 +

578259-578297 + PEMVVQACSLSY

Score = 0.027

&gt;NT\_027064.2

MGKGWEVYNRQDLQPEMVVQACSLSY\*

**FIGURE 15****HMMGENE FOR NT\_028428.2**

Peptide NAKISQAPW (SEQ ID NO:102, frame = 1)

Predictions :

290705-290780 +

296029-296147 + NAKISQAPW

Score = 0.091

&gt;NT\_028428.2

MDASVGHYPPKINTGMENQVPHVLASLWEAEVGESPEVRSSKPDWPRWQNPISTKNAKI  
SQAPW\***FIGURE 16****HMMGENE FOR NT\_019546.5**

Peptide NPMKIFEK (SEQ ID NO:67, frame = 1)

Predictions :

611472-611544 + NPMKIFEK

612968-613179 +

Score = 0.475

&gt;NT\_019546.5

MMLRNPMKIFEKRRKYIPQQKMLQK\*